☐ 1: P10719. ATP synthase beta...[gi:114562] NEW Links

```
LOCUS       ATPB_RAT                  529 aa            linear   ROD 15-JUN-2002
DEFINITION  ATP synthase beta chain, mitochondrial precursor.
ACCESSION   P10719
VERSION     P10719  GI:114562
DBSOURCE    swissprot: locus ATPB_RAT, accession P10719;
            class: standard.
            created: Jul 1, 1989.
            sequence updated: Apr 1, 1990.
            annotation updated: Jun 15, 2002.
            xrefs: gi: 601866, gi: 601867, gi: 205539, gi: 1374715, gi: 203032,
            gi: 203033, gi: 92350, gi: 92349, gi: 111746, pdb accession 1MAB
            xrefs (non-sequence databases): HSC-2DPAGE P10719, InterPro
            IPR000793, InterPro IPR004100, InterPro IPR000194, Pfam PF00006,
            Pfam PF00306, Pfam PF02874, PROSITE PS00152
KEYWORDS    ATP synthesis; CF(1); Hydrogen ion transport; Hydrolase;
            ATP-binding; Mitochondrion; Transit peptide; 3D-structure.
SOURCE      Rattus norvegicus.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (residues 1 to 529)
  AUTHORS   Boulet,D., Poirier,J. and Cote,C.
  TITLE     Studies on the biogenesis of the mammalian ATP synthase complex:
            isolation and characterization of a full-length cDNA encoding the
            rat F1-beta-subunit
  JOURNAL   Biochem. Biophys. Res. Commun. 159 (3), 1184-1190 (1989)
  MEDLINE   89193709
   PUBMED   2522775
  REMARK    SEQUENCE OF 1-60 FROM N.A.
REFERENCE   2  (residues 1 to 529)
  AUTHORS   Garboczi,D.N., Fox,A.H., Gerring,S.L. and Pedersen,P.L.
  TITLE     Beta subunit of rat liver mitochondrial ATP synthase: cDNA cloning,
            amino acid sequence, expression in Escherichia coli, and structural
            relationship to adenylate kinase
  JOURNAL   Biochemistry 27 (2), 553-560 (1988)
  MEDLINE   88163632
   PUBMED   2894849
  REMARK    SEQUENCE OF 58-529 FROM N.A.
REFERENCE   3  (residues 1 to 529)
  AUTHORS   Lee,Y.M., Chu,L.P. and Lee,S.C.
  TITLE     Molecular cloning of cDNA for the rat F1-ATPase beta subunit
  JOURNAL   Taiwan I Hsueh Hui Tsa Chih 87 (10), 933-938 (1988)
  MEDLINE   89198923
   PUBMED   2907347
  REMARK    SEQUENCE OF 172-529 FROM N.A.
REFERENCE   4  (residues 1 to 529)
```

AUTHORS Cretin,F., Baggetto,L.G., Denoroy,L. and Godinot,C.
TITLE N-terminal sequence of the rat liver beta-subunit in the mitochondrial ATPase-ATPsynthase
JOURNAL Biochem. Biophys. Res. Commun. 164 (3), 1165-1169 (1989)
MEDLINE 90073643
PUBMED 2531579
REMARK SEQUENCE OF 47-60.
REFERENCE 5 (residues 1 to 529)
AUTHORS Bianchet,M.A., Hullihen,J., Pedersen,P.L. and Amzel,L.M.
TITLE The 2.8-A structure of rat liver F1-ATPase: configuration of a critical intermediate in ATP synthesis/hydrolysis
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (19), 11065-11070 (1998)
MEDLINE 98409611
PUBMED 9736690
REMARK X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
COMMENT ----------

----------.
[FUNCTION] PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON GRADIENT ACROSS THE MEMBRANE. THE BETA CHAIN IS THE CATALYTIC SUBUNIT.
[CATALYTIC ACTIVITY] ATP + H(2)O + H(+)(In) = ADP + phosphate + H(+)(Out).
[SUBUNIT] F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0) HAS THREE MAIN SUBUNITS: A, B AND C.
[SUBCELLULAR LOCATION] Mitochondrial.
[SIMILARITY] BELONGS TO THE ATPASE ALPHA/BETA CHAINS FAMILY.

FEATURES	Location/Qualifiers
source	1..529 /organism="Rattus norvegicus" /db_xref="taxon:10116"
gene	1..529 /gene="ATP5B"
Protein	1..529 /gene="ATP5B" /product="ATP synthase beta chain, mitochondrial precursor" /EC_number="3.6.3.14"
Region	1..46 /gene="ATP5B" /region_name="Transit peptide" /note="MITOCHONDRION."
Region	47..529 /gene="ATP5B" /region_name="Mature chain" /note="ATP SYNTHASE BETA CHAIN."
Site	206..213 /gene="ATP5B" /site_type="np-binding" /note="ATP (BY SIMILARITY)."
Region	257..258 /gene="ATP5B" /region_name="Conflict" /note="NL -> KV (IN REF. 3)."

h cb hg e e e fcg c e e e b e e

```
     Region           429..430
                      /gene="ATP5B"
                      /region_name="Conflict"
                      /note="QD -> HV (IN REF. 3)."
ORIGIN
        1 mlslvgrvas asasgalrgl nplaalpqah lllrtapagv hpardyaaqs saapkagtat
       61 gqivavigav vdvqfdeglp pilnalevqg resrlvleva qhlgestvrt iamdgteglv
      121 rgqkvldsga pikipvgpet lgrimnvige pidergpikt kqfapihaea pefiemsveq
      181 eilvtgikvv dllapyakgg kiglfggagv gktvlimeli nnvakahggy svfagvgert
      241 regndlyhem iesgvinlkd atskvalvyg qmneppgara rvaltgltva eyfrdqegqd
      301 vllfidnifr ftqagsevsa llgripsavg yqptlatdmg tmqeritttk kgsitsvqai
      361 yvpaddltdp apattfahld attvlsraia elgiypavdp ldstsrimdp nivgsehydv
      421 argvqkilqd ykslqdiiai lgmdelseed kltvsrarki qrflsqpfqv aevftghmgk
      481 lvplketikg fqqilagdyd hlpeqafymv gpieeavaka dklaeehgs
//
```

Revised: July 5, 2002.

Aug 28 2002 15:52:55

h cb h g e e e fcg c e e e b e e

☐ **1:** BQ101922. ih87h08.x1 Melton...[gi:20134906] NEW Links

IDENTIFIERS

dbEST Id: **12071197**
EST name: ih87h08.x1
GenBank Acc: BQ101922
GenBank gi: 20134906

CLONE INFO
Clone Id: IMAGE:5939199 (3')
Source: University of Pennsylvania & Harvard University (HHMI) & Washington University (GSC)
Other ESTs on clone:ih87h08.y1
DNA type: cDNA

PRIMERS
Sequencing: -40UP from Gibco
PolyA Tail: Unknown

SEQUENCE

CCTTTTTTTTTTTTTTTGAGGGGTATATACTTTATTGAAAACTTTAAATACTCTTCAGAG
AGAACATCACATCTTCAATCAAGGCTCTTGTGTGGCCTGCATGGAAGGAAACCTGAGCTC
TCGCTTGATATGGAGAGATCAGTTGCAGTGCTGCCTTTGGCTGGAGTCCCTCACGACCCG
TGCTCTTCTGCCAGCTTATCAGCCTTTGCCACGGCTTCTTCAATGGGTCCCACCATGTAG
AAGGCTTGTTCTGGGAGATGGTCATATTCACCTGCTAAAATCTGCTGGAATCCTTTAATG
GTCTCCTTCAAGGGCACCAGCTTCCCCATGTGACCCGTGAAGACCTCAGCAACTTGGAAT
GGCTGAGACAAGAAGCGCTGTATCTTTCTTGCCCGGGACACAGTCAATTTATCTTCCTCA
GAAAGTTCATCCATACCCAAGATGGCAATGATGTCCTGGAGAGATTTGTAGTCCTGCAGG
ATTTTCTGCACTCCTCGGGCGACGTCATAATGCTCATTGCCAACAATGTTGGGATCCATA
ATTCGAGAGGTGGAGTCCAGTGGATCCACAGCTGGATAGATGCCCAACTCAGCAATAGCC
CGGGACAA

Quality: High quality sequence stops at base: 469

Entry Created: Apr 10 2002
Last Updated: Apr 10 2002

COMMENTS

Library was constructed by Dr. Douglas Melton DNA sequencing by: Washington University Genome Sequencing Center This clone is available royalty-free through LLNL; please contact the IMAGE consortium (info@image.llnl.gov) for further information

PUTATIVE ID Assigned by submitter
SW:ATPB_RAT P10719 ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR ;

LIBRARY

h cb hg e e e fcg c e e e b c e e e

Lib Name:	Melton Mouse E16 5 Pancreas Library 2 M16B2
Organism:	Mus musculus
Strain:	ICR
Sex:	Both
Organ:	Pancreas
Tissue type:	Total pancreas
Develop. stage:	Embryonic day 16.5
Lab host:	TOP10
Vector:	pBluescript II SK
R. Site 1:	NotI
R. Site 2:	SalI
Description:	Library constructed using SuperScript Plasmid Library kit (Life Technologies). cDNA made by oligo-dT priming.Size-selected by column fractionation; average insert size 1.06kb. Primary library, unamplified.

SUBMITTER

Name:	Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Lab:	Endocrine Pancreas Consortium
Institution:	Harvard University, Howard Hughes Medical Institute
Address:	Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
Tel:	617-495-1812
Fax:	617-495-8557
E-mail:	dmelton@biohp.harvard.edu

CITATIONS

Title:	Endocrine Pancreas Consortium
Authors:	Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner ,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin ,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko ,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R. , Tsagareishvili,R., Williams,T., Jackson,Y., Bowers,Y.
Year:	2000
Status:	Unpublished

MAP DATA

Revised: July 5, 2002.

h cb hg e e e fcg c e e e b c e e e